

J.F
Au 18/2
#13
3/4/96
OUE
3/01/96

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/249,671A

CRF Processing Date: 3/4/96
Edited by: JW
Verified by: JW (STIC staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other **ENTERED**

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

Other:

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

INPUT SET: S9110.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

INPUT SET: S9110.raw

47
48 (i) SEQUENCE CHARACTERISTICS:
49 (A) LENGTH: 25 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: both
52 (D) TOPOLOGY: unknown
53
54 (ii) MOLECULE TYPE: cDNA
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58 CGTCTTCAAG AATTCGAGAT TATCG 25
59
60 (2) INFORMATION FOR SEQ ID NO: 2:
61
62 (i) SEQUENCE CHARACTERISTICS:
63 (A) LENGTH: 56 base pairs
64 (B) TYPE: nucleic acid
65 (C) STRANDEDNESS: both
66 (D) TOPOLOGY: unknown
67
68 (ii) MOLECULE TYPE: cDNA
69
70
71
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73
74 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCCT TACTTCTTAA ACTTTC 56
75
76 (2) INFORMATION FOR SEQ ID NO: 3:
77
78 (i) SEQUENCE CHARACTERISTICS:
79 (A) LENGTH: 35 base pairs
80 (B) TYPE: nucleic acid
81 (C) STRANDEDNESS: both
82 (D) TOPOLOGY: unknown
83
84 (ii) MOLECULE TYPE: cDNA
85
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89
90 ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC 35
91
92 (2) INFORMATION FOR SEQ ID NO: 4:
93
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 34 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: both
98 (D) TOPOLOGY: unknown
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 16:50:30

INPUT SET: S9110.raw

100 (ii) MOLECULE TYPE: cDNA
101
102
103
104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105
106 GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG 34
107
108 (2) INFORMATION FOR SEQ ID NO: 5:
109
110 (i) SEQUENCE CHARACTERISTICS:
111 (A) LENGTH: 165 amino acids
112 (B) TYPE: amino acid
113 (D) TOPOLOGY: linear
114
115 (ii) MOLECULE TYPE: protein
116
117
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
119
120 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
121 1 5 10 15
122 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
123 20 25 30
124
125 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
126 35 40 45
127
128 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
129 50 55 60
130
131 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
132 65 70 75 80
133
134 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
135 85 90 95
136
137 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
138 100 105 110
139
140 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
141 115 120 125
142
143 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
144 130 135 140
145
146 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
147 145 150 155 160
148
149 Leu Arg Ser Lys Glu
150 165
151
152

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 16:50:33

INPUT SET: S9110.raw

153
 154 (2) INFORMATION FOR SEQ ID NO: 6:
 155
 156 (i) SEQUENCE CHARACTERISTICS:
 157 (A) LENGTH: 495 base pairs
 158 (B) TYPE: nucleic acid
 159 (C) STRANDEDNESS: both
 160 (D) TOPOLOGY: unknown
 161
 162 (ii) MOLECULE TYPE: cDNA
 163
 164
 165 (ix) FEATURE:
 166 (A) NAME/KEY: CDS
 167 (B) LOCATION: 1..495
 168
 169
 170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 171
 172 TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGC AGG AGG ACC TTG ATG 48
 173 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 174 1 5 10 15
 175
 176 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC 96
 177 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 178 20 25 30
 179
 180 AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA 144
 181 Arg Arg Asp Phe Gly Phe Pro Gln Glu Phe Gly Asn Gln Phe Gln
 182 35 40 45
 183
 184 AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC 192
 185 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 186 50 55 60
 187
 188 AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC 240
 189 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 190 65 70 75 80
 191
 192 CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA 288
 193 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 194 85 90 95
 195
 196 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG 336
 197 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 198 100 105 110
 199
 200 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC 384
 201 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 202 115 120 125
 203
 204 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA 432
 205 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg

INPUT SET: S9110.raw

206	130	135	140	
207				
208	GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT			480
209	Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser			
210	145	150	155	160
211				
212	TTA AGA AGT AAG GAA			495
213	Leu Arg Ser Lys Glu			
214	165			
215				
216				
217				
218	(2) INFORMATION FOR SEQ ID NO: 7:			
219				
220	(i) SEQUENCE CHARACTERISTICS:			
221	(A) LENGTH: 869 base pairs			
222	(B) TYPE: nucleic acid			
223	(C) STRANDEDNESS: both			
224	(D) TOPOLOGY: unknown			
225				
226	(ii) MOLECULE TYPE: cDNA			
227				
228				
229				
230	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:			
231				

232	GAATTCCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG	60
233		
234	TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTGAC	120
235		
236	GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA	180
237		
238	AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACGG CCGAGACTTA TAGTCGCTTT	240
239		
240	GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC	300
241		
242	GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT	360
243		
244	CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG	420
245		
246	AGAATCTCTC TTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTC CCAGGAGGAG	480
247		
248	TTGGCAACC AGTTCCAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG	540
249		
250	ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC	600
251		
252	AAATTCTACA CTGAACCTCA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG	660
253		
254	GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC	720
255		
256	TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT	780
257		
258	GTCAGAGCAG AAATCATGAG ATCTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA	840

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:01

INPUT SET: S9110.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

SEQUENCE LISTING

1
2
3 (1) General Information:4
5 (i) APPLICANTS: Hauptmann, R.
6 Falkner, E.
7 Bodo, G.
8 VoÃ, T.
9 Maurer-Fogy, I.*Wanted*
Does Not Comply
Corrected Diskette Needed10
11 (ii) TITLE OF INVENTION: Process for Preparing and Purifying
12 alpha-Interferon13
14 (iii) NUMBER OF SEQUENCES: 1115
16 (iv) CORRESPONDENCE ADDRESS:17 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
18 (B) STREET: 1100 New York Avenue, Suite 600
19 (C) CITY: Washington
20 (D) STATE: D.C.
21 (E) COUNTRY: U.S.A.
22 (F) ZIP: 2000523
24 (v) COMPUTER READABLE FORM:25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)29
30 (vi) CURRENT APPLICATION DATA:31 (A) APPLICATION NUMBER: 08/249,671
32 (B) FILING DATE: 26-MAY-1994
33 (C) CLASSIFICATION:34
35 (viii) ATTORNEY/AGENT INFORMATION:36 (A) NAME: Esmond, Robert W.
37 (B) REGISTRATION NUMBER: 32,893
38 (C) REFERENCE/DOCKET NUMBER: 0652.135000039
40 (ix) TELECOMMUNICATION INFORMATION:41 (A) TELEPHONE: (202) 371-2600
42 (B) TELEFAX: (202) 371-254043
44
45

INPUT SET: S9110.raw

ERRORED SEQUENCES FOLLOW:

154 (2) INFORMATION FOR SEQ ID NO: 6:

155

156 (i) SEQUENCE CHARACTERISTICS:
--> 157 (A) LENGTH: 495 base pairs
158 (B) TYPE: nucleic acid
159 (C) STRANDEDNESS: both
160 (D) TOPOLOGY: unknown

161

162 (ii) MOLECULE TYPE: cDNA

163

164

165 (ix) FEATURE:

166 (A) NAME/KEY: CDS
167 (B) LOCATION: 1..495

168

169

170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

171

172 TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGC AGG ACC TTG ATG
173 48174 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
175 1 5 10 15

176

177 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC
178 96179 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
180 20 25 30

181

182 AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA
183 144184 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
185 35 40 45

186

187 AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC
188 192189 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
190 50 55 60

191

192 AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC
193 240194 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
195 65 70 75 80

196

197 CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA
198 288199 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
200 85 90 95

INPUT SET: S9110.raw

201
202 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
203 336
204 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
205 100 105 110
206
207 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
208 384
209 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
210 115 120 125
211
212 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
213 432
214 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
215 130 135 140
216
217 GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
218 480
219 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
220 145 150 155 160
221
222 TTA AGA AGT AAG GAA
223 495
224 Leu Arg Ser Lys Glu
225 165
226
227
228

229 (2) INFORMATION FOR SEQ ID NO: 7:
230

231 (i) SEQUENCE CHARACTERISTICS:

232 (A) LENGTH: 869 base pairs
233 (B) TYPE: nucleic acid
234 (C) STRANDEDNESS: both
235 (D) TOPOLOGY: unknown

236 (ii) MOLECULE TYPE: cDNA

237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
238
239
240

241 GAATTCTGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
242
243 60

244
245 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTGAC
246 120

247
248 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
249 180

250
251 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACGG CCGAGACTTA TAGTCGCTTT
252

INPUT SET: S9110.raw

253 240
254
255 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC
256 300
257
258 GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT
259 360
260
261 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG
262 420
263
264 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG
265 480
266
267 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG
268 540
269
270 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC
271 600
272
273 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG
274 660
275
276 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC
277 720
278
279 TTCCAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT
280 780
281
282 GTCAGAGCAG AAATCATGAG ATCTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA
283 840
284
285 AGTAAGGAAT GATAACGATC GTAACTGCA
286 869
287

288 (2) INFORMATION FOR SEQ ID NO: 8:
289

290 (i) SEQUENCE CHARACTERISTICS:
291 (A) LENGTH: 1177 base pairs
292 (B) TYPE: nucleic acid
293 (C) STRANDEDNESS: both
294 (D) TOPOLOGY: unknown
295

296 (ii) MOLECULE TYPE: cDNA
297

298 (ix) FEATURE:
299 (A) NAME/KEY: CDS
300 (B) LOCATION: 286..873
301 (D) OTHER INFORMATION: /function= "Cytokine"
302 /product= "Interferon-omegal"
303
304

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:09

INPUT SET: S9110.raw

305 (ix) FEATURE:
306 (A) NAME/KEY: mat_peptide
307 (B) LOCATION: 355..873
308 (D) OTHER INFORMATION: /function= "Cytokine"
309 /product= "Interferon-omega"
310
311 (ix) FEATURE:
312 (A) NAME/KEY: sig_peptide
313 (B) LOCATION: 286..354
314 (D) OTHER INFORMATION: /product= "ST II Leader"
315
316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
317
318 GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
319 60
320
321 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCGTGAC
322 120
323
324 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
325 180
326
327 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACCGG CCGAGACTTA TAGTCGCTTT
328 240
329
330 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
331 294
332 Met Lys Lys
333 -23
334
335 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
336 342
337 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
338 -20 -15 -10 -5
339
340 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG
341 390
342 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
343 1 5 10
344
345 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG
346 438
347 Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
348 15 20 25
349
350 TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA
351 486
352 Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
353 30 35 40
354
355 GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG
356 534
357 Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:12

INPUT SET: S9110.raw

358	45	50	55	60
359				
360	CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC			
361	582			
362	Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala			
363	65	70	75	
364				
365	TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA			
366	630			
367	Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln			
368	80	85	90	
369				
370	CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA			
371	678			
372	Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu			
373	95	100	105	
374				
375	TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC			
376	726			
377	Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe			
378	110	115	120	
379				
380	CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC			
381	774			
382	Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala			
383	125	130	135	140
384				
385	TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA			
386	822			
387	Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr			
388	145	150	155	
389				
390	AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT			
391	870			
392	Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser			
393	160	165	170	
394				
395	TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT			
396	930			
397				
398	TCAAAAGACT CTTATTCGG CTTAACACAG AGAATTGACT GAATTAGTTC TGCAAATACT			
399	990			
400				
401	TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGC ATCAGTCCCT			
402	1050			
403				
404	AAGATGTTAT TTATTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT			
405	1110			
406				
407	TATATTCTTA TATAACAAAT GTTTGCCATT ACATTGTATT AAGATAACAA AACATGTTCA			
408	1170			
409				
410	GGATCCA			

INPUT SET: S9110.raw

411 1177
412
413464 (2) INFORMATION FOR SEQ ID NO: 10:
465466 (i) SEQUENCE CHARACTERISTICS:
467 (A) LENGTH: 879 base pairs
468 (B) TYPE: nucleic acid
469 (C) STRANDEDNESS: both
470 (D) TOPOLOGY: unknown
471472 (ii) MOLECULE TYPE: cDNA
473
474
475476 (ix) FEATURE:
477 (A) NAME/KEY: CDS
478 (B) LOCATION: 286..852
479480 (ix) FEATURE:
481 (A) NAME/KEY: mat_peptide
482 (B) LOCATION: 355..852
483 (D) OTHER INFORMATION: /function= "Cytokine"
484 /product= "Interferon-alpha-2c"
485486 (ix) FEATURE:
487 (A) NAME/KEY: sig_peptide
488 (B) LOCATION: 286..354
489 (D) OTHER INFORMATION: /product= "ST II Leader"
490
491492 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
493494 GAATTCTGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
495 60496 TTGATTGATC AGGTAGAGGG GCGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCCTGAC
497 120498 GACGATAACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
499 180500 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACCGG CCGAGACTTA TAGTCGCTTT
501 240502 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
503 294Met Lys Lys
-23508
509
510
511 AAT ATC GCA TTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
512 342

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:16

INPUT SET: S9110.raw

513 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
 514 -20 -15 -10 -5
 515
 516 AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG
 517 390
 518 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
 519 1 5 10
 520
 521 AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC
 522 438
 523 Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
 524 15 20 25
 525
 526 TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC
 527 486
 528 Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
 529 30 35 40
 530
 531 AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC
 532 534
 533 Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
 534 45 50 55 60
 535
 536 CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG
 537 582
 538 Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
 539 65 70 75
 540
 541 GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG
 542 630
 543 Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
 544 80 85 90
 545
 546 AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT
 547 678
 548 Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
 549 95 100 105
 550
 551 CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA
 552 726
 553 Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
 554 110 115 120
 555
 556
 557
 558 AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG
 559 774
 560 Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
 561 125 130 135 140
 562
 563 GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC
 564 822
 565 Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:18

INPUT SET: S9110.raw

566	145	150	155
567			
568	TTG CAA GAA AGT TTA AGA AGT AAG GAA	TGATAACGAT CGTAACTGCA	
569	869		
570	Leu Gln Glu Ser Leu Arg Ser Lys Glu		
571	160	165	
572			
573	GAAGCTTAAT		
574	879		
575			

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/249,671ADATE: 03/04/96
TIME: 15:06:19**INPUT SET: S9110.raw**

Line	Error	Original Text
157	Entered (495) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs
232	Entered (869) and Calc. Seq. Length (0) differ	(A) LENGTH: 869 base pairs
291	Entered (1177) and Calc. Seq. Length (0) differ	(A) LENGTH: 1177 base pairs
467	Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 879 base pairs